Nucleotide and Amino Acid Sequence of AIM-I

```
     GGCACGAGCGGCTGCCTGGCTGACTTACAGCAGTCAGACTCTGACAGGTTCATGGCTATG
-51  -+---------+---------+---------+---------+---------+---------+--------  8
     CCGTGCTCGCCGACGGACCGACTGAATGTCGTCAGTCTGAGACTGTCCAAGTACCGATAC
-16                                                      M  A  M    3

     ATGGAGGTCCAGGGGGGACCCAGCCTGGGACAGACCTGCGTGCTGATCGTGATCTTCACA
  9  -+---------+---------+---------+---------+---------+---------+--------  68
     TACCTCCAGGTCCCCCCTGGGTCGGACCCTGTCTGGACGCACGACTAGCACTAGAAGTGT
  4  M  E  V  Q  G  G  P  S  L  G  Q  T  C  V  L  I  V  I  F  T    23

     GTGCTCCTGCAGTCTCTCTGTGTGGCTGTAACTTACGTGTACTTTACCAACGAGCTGAAG
 69  -+---------+---------+---------+---------+---------+---------+--------  128
     CACGAGGACGTCAGAGAGACACACCGACATTGAATGCACATGAAATGGTTGCTCGACTTC
 24  V  L  L  Q  S  L  C  V  A  V  T  Y  V  Y  F  T  N  E  L  K    43

     CAGATGCAGGACAAGTACTCCAAAAGTGGCATTGCTTGTTTCTTAAAAGAAGATGACAGT
129  -+---------+---------+---------+---------+---------+---------+--------  188
     GTCTACGTCCTGTTCATGAGGTTTTCACCGTAACGAACAAAGAATTTTCTTCTACTGTCA
 44  Q  M  Q  D  K  Y  S  K  S  G  I  A  C  F  L  K  E  D  D  S    63

     TATTGGGACCCCAATGACGAAGAGAGTATGAACAGCCCCTGCTGGCAAGTCAAGTGGCAA
189  -+---------+---------+---------+---------+---------+---------+--------  248
     ATAACCCTGGGGTTACTGCTTCTCTCATACTTGTCGGGGACGACCGTTCAGTTCACCGTT
 64  Y  W  D  P  N  D  E  E  S  M  N  S  P  C  W  Q  V  K  W  Q    83

     CTCCGTCAGCTCGTTAGAAAGATGATTTTGAGAACCTCTGAGGAAACCATTTCTACAGTT
249  -+---------+---------+---------+---------+---------+---------+--------  308
     GAGGCAGTCGAGCAATCTTTCTACTAAAACTCTTGGAGACTCCTTTGGTAAAGATGTCAA
 84  L  R  Q  L  V  R  K  M  I  L  R  T  S  E  E  T  I  S  T  V    103

     CAAGAAAAGCAACAAAATATTTCTCCCCTAGTGAGAGAAAGAGGTCCTCAGAGAGTAGCA
309  -+---------+---------+---------+---------+---------+---------+--------  368
     GTTCTTTTCGTTGTTTTATAAAGAGGGGATCACTCTCTTTCTCCAGGAGTCTCTCATCGT
104  Q  E  K  Q  Q  N  I  S  P  L  V  R  E  R  G  P  Q  R  V  A    123

     GCTCACATAACTGGGACCAGAGGAAGAAGCAACACATTGTCTTCTCCAAACTCCAAGAAT
369  -+---------+---------+---------+---------+---------+---------+--------  428
     CGAGTGTATTGACCCTGGTCTCCTTCTTCGTTGTGTAACAGAAGAGGTTTGAGGTTCTTA
124  A  H  I  T  G  T  R  G  R  S  N  T  L  S  S  P  N  S  K  N    143

     GAAAAGGCTCTGGGCCGCAAAATAAACTCCTGGGAATCATCAAGGAGTGGGCATTCATTC
429  -+---------+---------+---------+---------+---------+---------+--------  488
     CTTTTCCGAGACCCGGCGTTTTATTTGAGGACCCTTAGTAGTTCCTCACCCGTAAGTAAG
144  E  K  A  L  G  R  K  I  N  S  W  E  S  S  R  S  G  H  S  F    163
```

FIG.1A

```
      CTGAGCAACTTGCACTTGAGGAATGGTGAACTGGTCATCCATGAAAAAGGGTTTTACTAC
489   -+---------+---------+---------+---------+---------+---------  548
      GACTCGTTGAACGTGAACTCCTTACCACTTGACCAGTAGGTACTTTTTCCCAAAATGATG
164   L  S  N  L  H  L  R  N  G  E  L  V  I  H  E  K  G  F  Y  Y    183

      ATCTATTCCCAAACATACTTTCGATTTCAGGAGGAAATAAAAGAAAACACAAAGAACGAC
549   -+---------+---------+---------+---------+---------+---------  608
      TAGATAAGGGTTTGTATGAAAGCTAAAGTCCTCCTTTATTTTCTTTTGTGTTTCTTGCTG
184   I  Y  S  Q  T  Y  F  R  F  Q  E  E  I  K  E  N  T  K  N  D    203

      AAACAAATGGTCCAATATATTTACAAATACACAAGTTATCCTGACCCTATATTGTTGATG
609   -+---------+---------+---------+---------+---------+---------  668
      TTTGTTTACCAGGTTATATAAATGTTTATGTGTTCAATAGGACTGGGATATAACAACTAC
204   K  Q  M  V  Q  Y  I  Y  K  Y  T  S  Y  P  D  P  I  L  L  M    223

      AAAAGTGCTAGAAATAGTTGTTGGTCTAAAGATGCAGAATATGGACTCTATTCCATCTAT
669   -+---------+---------+---------+---------+---------+---------  728
      TTTTCACGATCTTTATCAACAACCAGATTTCTACGTCTTATACCTGAGATAAGGTAGATA
224   K  S  A  R  N  S  C  W  S  K  D  A  E  Y  G  L  Y  S  I  Y    243

      CAAGGGGGAATATTTGAGCTTAAGGAAAATGACAGAATTTTTGTTTCTGTAACAAATGAG
729   -+---------+---------+---------+---------+---------+---------  788
      GTTCCCCCTTATAAACTCGAATTCCTTTTACTGTCTTAAAAACAAAGACATTGTTTACTC
244   Q  G  G  I  F  E  L  K  E  N  D  R  I  F  V  S  V  T  N  E    263

      CACTTGATAGACATGGACCATGAAGCCAGTTTTTTCGGGGCCTTTTTAGTTGGCTAACTG
789   -+---------+---------+---------+---------+---------+---------  848
      GTGAACTATCTGTACCTGGTACTTCGGTCAAAAAAGCCCCGGAAAAATCAACCGATTGAC
264   H  L  I  D  M  D  H  E  A  S  F  F  G  A  F  L  V  G          281

      ACCTGGAAAGAAAAAGCAATAACCTCAAAGTGACTATTCAGTTTTCAGGATGATACACTA
849   -+---------+---------+---------+---------+---------+---------  908
      TGGACCTTTCTTTTTCGTTATTGGAGTTTCACTGATAAGTCAAAAGTCCTACTATGTGAT

      TGAAGATGTTTCAAAAAATCTGACCAAAACAAACAAACAGAAAACAGAAAACAAAAAAAC
909   -+---------+---------+---------+---------+---------+---------  968
      ACTTCTACAAAGTTTTTTAGACTGGTTTTGTTTGTTTGTCTTTTGTCTTTTGTTTTTTTG

      CTCTATGCAATCTGAGTAGAGCAGCCACAACCAAAAAATTCTACAACACACACTGTTCTG
969   -+---------+---------+---------+---------+---------+---------  1028
      GAGATACGTTAGACTCATCTCGTCGGTGTTGGTTTTTTAAGATGTTGTGTGTGACAAGAC

      AAAGTGACTCACTTATCCCAAGAAAATGAAATTGCTGAAAGATCTTTCAGGACTCTACCT
1029  -+---------+---------+---------+---------+---------+---------  1088
      TTTCACTGAGTGAATAGGGTTCTTTTACTTTAACGACTTTCTAGAAAGTCCTGAGATGGA

      CATATCAGTTTGCTAGCAGAAATCTAGAAGACTGTCAGCTTCCAAACATTAATGCAATGG
1089  -+---------+---------+---------+---------+---------+---------  1148
      GTATAGTCAAACGATCGTCTTTAGATCTTCTGACAGTCGAAGGTTTGTAATTACGTTACC
```

FIG. 1B

```
      TTAACATCTTCTGTCTTTATAATCTACTCCTTGTAAAGACTGTAGAAGAAAGCGCAACAA
1149  -+---------+---------+---------+---------+---------+---------+--------  1208
      AATTGTAGAAGACAGAAATATTAGATGAGGAACATTTCTGACATCTTCTTTCGCGTTGTT

      TCCATCTCTCAAGTAGTGTATCACAGTAGTAGCCTCCAGGTTTCCTTAAGGGACAACATC
1209  -+---------+---------+---------+---------+---------+---------+--------  1268
      AGGTAGAGAGTTCATCACATAGTGTCATCATCGGAGGTCCAAAGGAATTCCCTGTTGTAG

      CTTAAGTCAAAAGAGAGAAGAGGCACCACTAAAAGATCGCAGTTTGCCTGGTGCAGTGGC
1269  -+---------+---------+---------+---------+---------+---------+--------  1328
      GAATTCAGTTTTCTCTCTTCTCCGTGGTGATTTTCTAGCGTCAAACGGACCACGTCACCG

      TCACACCTGTAATCCCAACATTTTGGGAACCCAAGGTGGGTAGATCACGAGATCAAGAGA
1329  -+---------+---------+---------+---------+---------+---------+--------  1388
      AGTGTGGACATTAGGGTTGTAAAACCCTTGGGTTCCACCCATCTAGTGCTCTAGTTCTCT

      TCAAGACCATAGTGACCAACATAGTGAAACCCCATCTCTACTGAAAGTGCAAAAATTAGC
1389  -+---------+---------+---------+---------+---------+---------+--------  1448
      AGTTCTGGTATCACTGGTTGTATCACTTTGGGGTAGAGATGACTTTCACGTTTTTAATCG

      TGGGTGTGTTGGCACATGCCTGTAGTCCCAGCTACTTGAGAGGCTGAGGCAGGAGAATCG
1449  -+---------+---------+---------+---------+---------+---------+--------  1508
      ACCCACACAACCGTGTACGGACATCAGGGTCGATGAACTCTCCGACTCCGTCCTCTTAGC

      TTTGAACCCGGGAGGCAGAGGTTGCAGTGTGGTGAGATCATGCCACTACACTCCAGCCTG
1509  -+---------+---------+---------+---------+---------+---------+--------  1568
      AAACTTGGGCCCTCCGTCTCCAACGTCACACCACTCTAGTACGGTGATGTGAGGTCGGAC

      GCGACAGAGCGAGACTTGGTTTC
1569  -+---------+---------+-  1591
      CGCTGTCTCGCTCTGAACCAAAG
```

FIG.1C

Alignment of AIM-I to Human Fas Ligand
(Similarity = 48.594 % Identity = 22.892 %)

```
  4 MEVQGGPSLGQTCVLIVIFTVL.................LQSLCVAVTYV 36
    ::  ::..::.....::.. | :                 |.. ..:....
 15 vdssasspwappgtvlpcptsvprrpgqrrpppppppppplpppppppplp 64

 37 YFTNELKQMQDKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQ 86
     :.  |..:..: ..|.  |:|     :    .  ::. . :|: ::|..
 65 plp..lpplkkrgnhstglcllvm..ffmvlvalvglglgmfql.fhlqk 109

 87 LVRKMILRTSEETISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTL 136
     : .:  .||:  ...  ||| . .. ..|: . | .||:|   |:||.
110 elaelrestsqmhtasslekqighpspppekkelrkvahlt...gksnsr 156

137 SSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYS 186
    | | ..::.             |  :||.:..:.|:|||:|.|:|::||
157 smplewedty.............givllsgvkykkgglvinetglyfvys 193

187 QTYFRFQEEIKENTKNDKQMVQYIYKYTS.YPDPILLMKSARNSCWSKDA 235
    ..|||      :.. |: .: : :|. .| ||:.:::|.: . |: ..:.
194 kvyfr......gqscnnlplshkvymrnskypqdlvmmegkmmsycttgq 237

236 EYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 280
     ::  | | |::|:|...|:::|.|.:  |::::....||| : :
238 mwar.ssylgavfnltsadhlyvnvselslvnfeesqtffglykl 281
```

FIG.2

Alignment Report of AIM-I, hFas Ligand, TNF-α and TNF-β
by Clustal Method with PAM250 Residue Weight Table

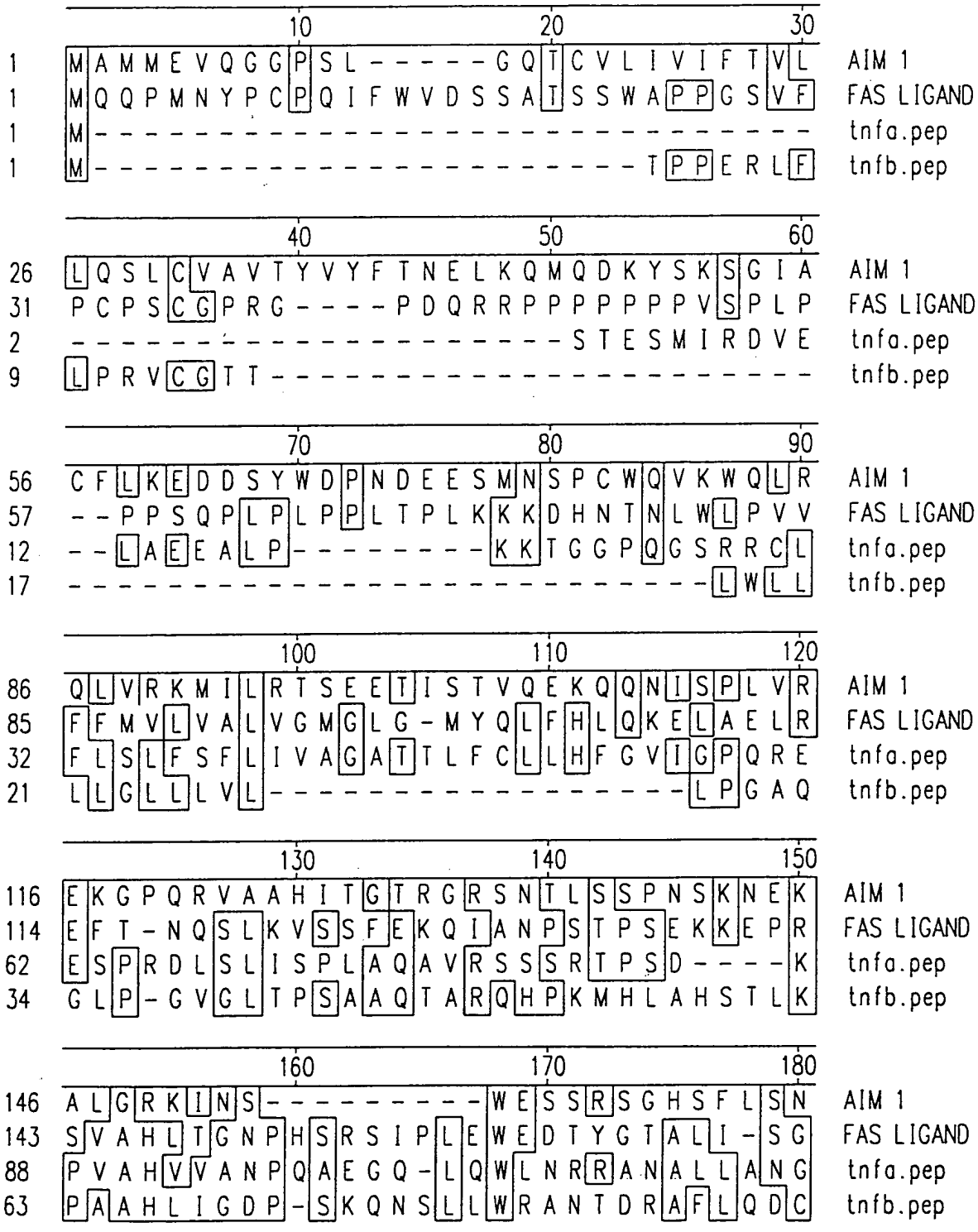
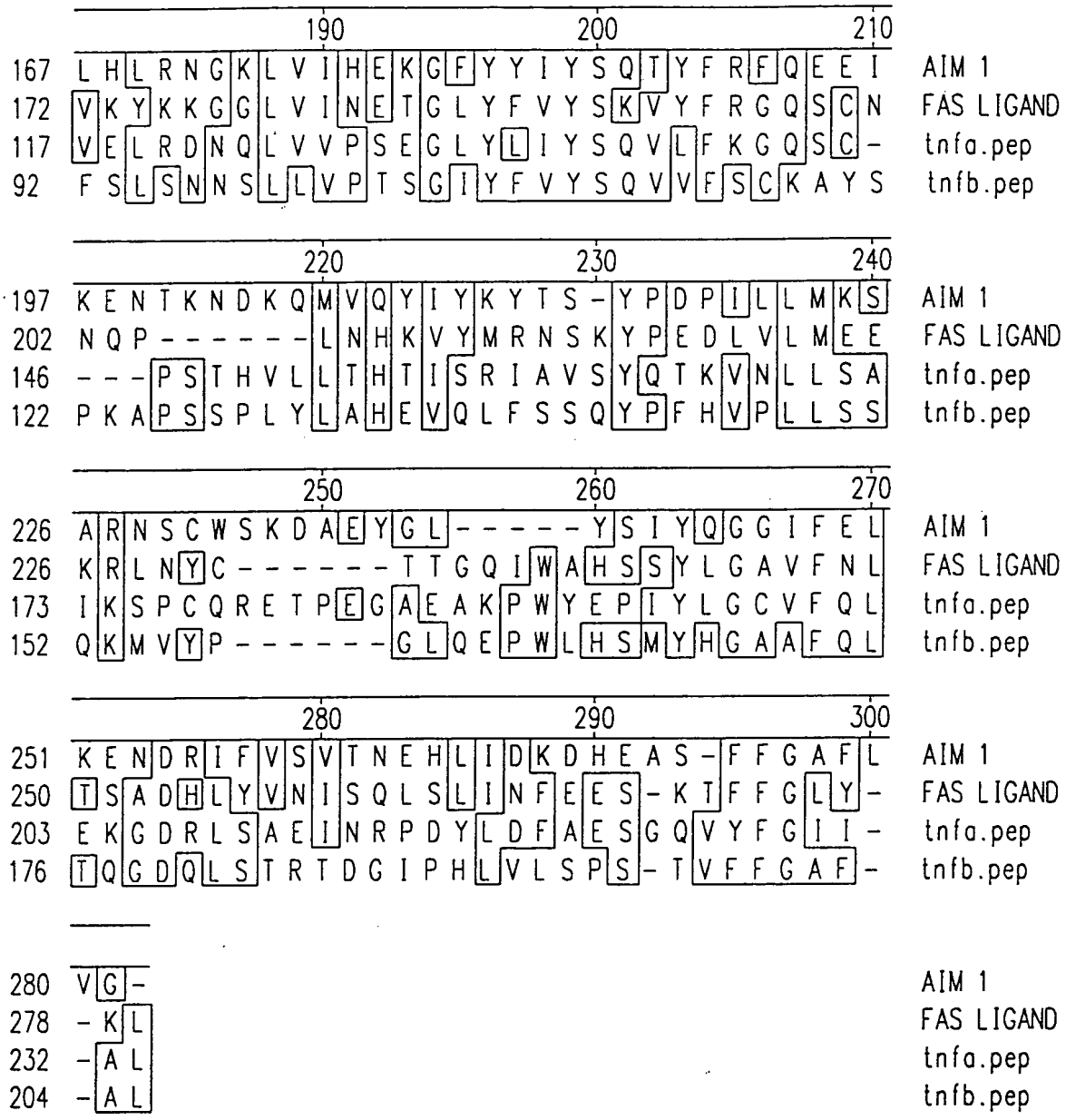


FIG.3A



Decoration 'Decoration #1': Box residues that match the Consensus within 2 distance units.

FIG.3B

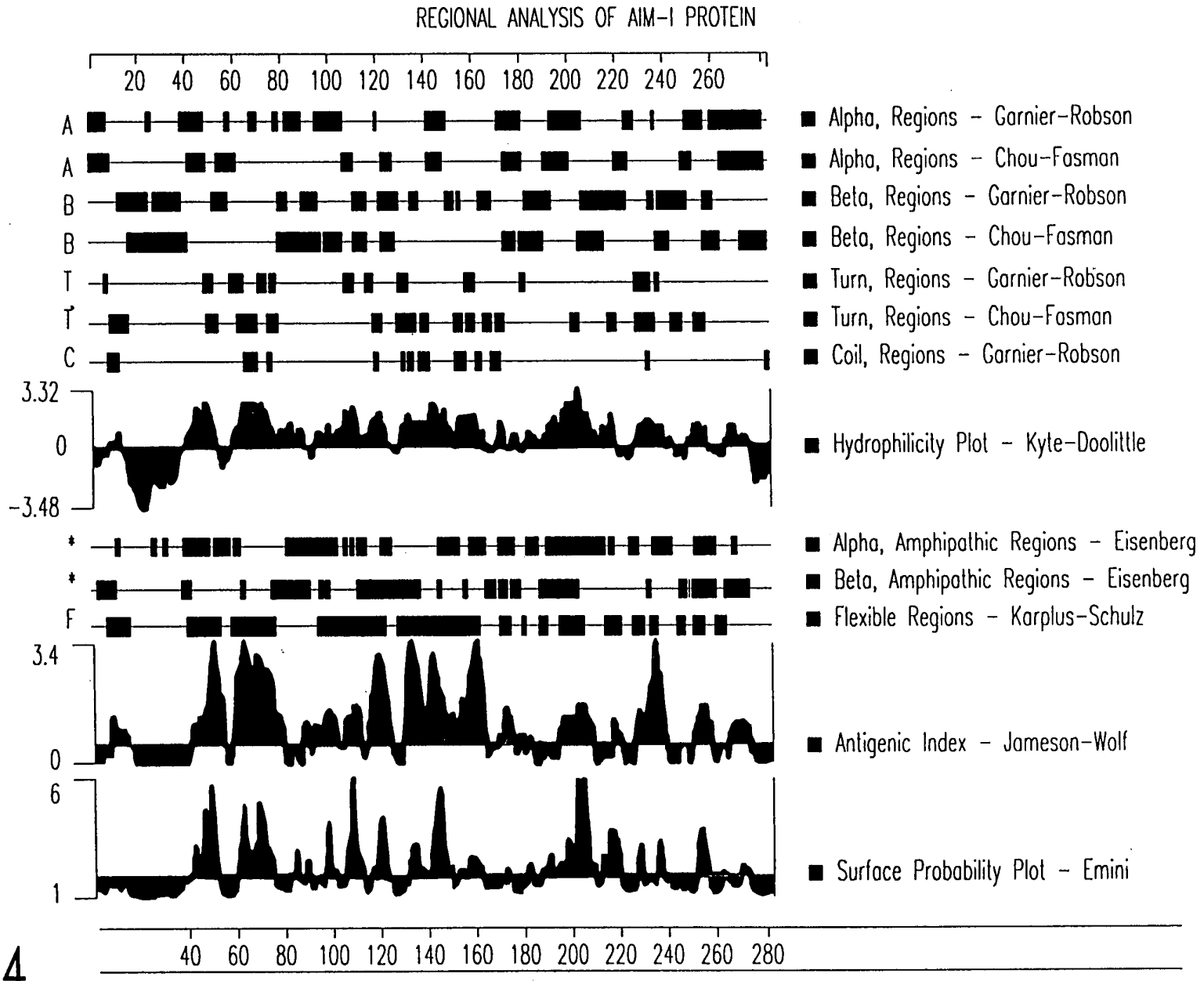

REGIONAL ANALYSIS OF AIM-1 PROTEIN
20 40 60 80 100 120 140 160 180 200 220 240 260
A
A
B
B
T
T
C
Alpha, Regions - Garnier-Robson
Alpha, Regions - Chou-Fasman
Beta, Regions - Garnier-Robson
Beta, Regions - Chou-Fasman
Turn, Regions - Garnier-Robson
Turn, Regions - Chou-Fasman
Coil, Regions - Garnier-Robson
3.32
0
-3.48
Hydrophilicity Plot - Kyte-Doolittle
*
*
F
Alpha, Amphipathic Regions - Eisenberg
Beta, Amphipathic Regions - Eisenberg
Flexible Regions - Karplus-Schulz
3.4
0
Antigenic Index - Jameson-Wolf
6
1
Surface Probability Plot - Emini
40 60 80 100 120 140 160 180 200 220 240 260 280

FIG.4